

Qy 1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557  
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 Db 36621 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 36562

Qy 1558 TTGCTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 1617  
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 Db 36561 TTGCTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 36502

Qy 1618 AGGACC 1623  
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 Db 36501 AGGACC 36496

## SR Gapped comparison A

RESULT 3  
 HSU32674

LOCUS HSU32674 1293 bp DNA PRI 05-JUN-1996  
 DEFINITION Human orphan receptor GPR9 (GPR9) gene, partial cds.  
 ACCESSION U32674  
 VERSION U32674.1 GI:1002740  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1293)  
 AUTHORS Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,  
 Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.  
 and Docherty,J.M.  
 TITLE Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,  
 and GPR14, encoding receptors related to interleukin 8,  
 neuropeptide Y, and somatostatin receptors  
 JOURNAL Genomics 29 (2), 335-344 (1995)  
 MEDLINE 96115583

REFERENCE 2 (bases 1 to 1293)  
 AUTHORS Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,  
 Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.  
 and Docherty,J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology,  
 University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario M5S  
 1A8, Canada

FEATURES  
 source Location/Qualifiers  
 1..1293  
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 /gene="GPR9"  
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 /gene="GPR9"  
 CDS <109..1203  
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 /db\_xref="GI:1002741"  
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 LNFDR AFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSD TFLHLAVADTLLVLT  
 PLWAVDAAVQWVFGSLCKVAGALFNIFYAGALLACISFDRLNIVHATQLYRRGP  
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 GFLPLLV MAYCYAHILAVLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVLVDIL  
 MDLGALARNCGRESRVDVAKSVTSGLG YMHCCLNPLLYAFVGVKFRERMWMLLLRLGC  
 PNQRGLQRQPSSSRDSSWSETSEASYSGL"

BASE COUNT 201 a 458 c 357 g 277 t  
 ORIGIN

Query Match 71.1%; Score 1187.2; DB 66; Length 1293;  
Best Local Similarity 98.9%; Pred. No. 1.5e-184;  
Matches 1195; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	58	CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG	117
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Qy	118	CCGCCCTCCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTCGT	177
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Qy	178	GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC	237
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Qy	238	CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG	297
Db	266	CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG	325
Qy	298	TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACCTTCCTGCTCCACCTAGCTG	357
Db	326	TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACCTTCCTGCTCCACCTAGCTG	385
Qy	358	TAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT	417
Db	386	TAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT	445
Qy	418	GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG	477
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Qy	478	CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCA	537
Db	506	CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCA	565
Qy	538	CCCAGCTCTACCGCCGGGGGCCCGCCCGCGTGAACCTCAGCTGCCTGGCTGTCTGGG	597
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Qy	598	GGCTCTGCCTGCTTTTCGCCCTCCAGACTTCATCTTCTGTGCGGCCACCACGACGAGC	657
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Qy	718	TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCC	777
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Qy	778	ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGG	837
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Qy	838	TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGTCTGG	897
Db	866	TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGTCTGG	925
Qy	898	TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG	957
Db	926	TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG	985
Qy	958	ACGTGGCCAAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC	1017
Db	986	ACGTGGCCAAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC	1045
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# Sequence comparison A

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Db      1046 TCTATGCCTTTGTAGGGGTCAAGTTCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1105
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Db      1106 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTATCCT 1165
Qy      1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197
Db      1166 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1225
Qy      1198 TCGCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257
Db      1226 TCGCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1285
Qy      1258 CTCCCCAA 1265
Db      1286 CTCCCCAA 1293

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```

RESULT 1
V26557
ID V26557 standard; DNA; 1670 BP.
XX
AC V26557;
XX
DT 14-AUG-1998 (first entry)
XX
DE Human IP-10/Mig receptor CXCR3 gene.
XX
KW ds; chemokine receptor; cellular signal; treatment; T cell;
KW inflammatory disease; antitumour; antiviral.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 69..1175
FT /*tag= a
FT /product= "IP-10/Mig receptor CXCR3"
FT polyA_signal 1534..1539
FT /*tag= b
FT polyA_site 1624..1670
FT /*tag= c
XX
PN WO9811218-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US15915.
XX
PR 31-MAR-1997; 97US-0829839.
PR 10-SEP-1996; 96US-0709838.
XX
PA (KOCH-) KOCHER INST THEODOR.
PA (LEUK-) LEUKOSITE INC.
XX
PI Loetscher M, Mackay CR, Moser B, Qin S;
XX
DR WPI; 1998-207381/18.
DR P-PSDB; W54371.
XX
PT DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT which, are useful for treatment of inflammation or in anti-tumour or
PT anti-viral therapy
XX
PS Claim 6; Fig 1; 137pp; English.
XX
CC The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein
CC which can selectively bind one or more chemokines and can mediate
CC cellular signalling and/or a cellular response in response. Inhibitors

```

CC and promoters of mammalian CXCR3 can be detected and identified using  
CC host cells expressing CXCR3. CXCR3 inhibitors can be used for treatment  
CC of inflammatory diseases which are T cell mediated. CXCR3 promoters are  
CC useful for antitumour or antiviral therapy.

XX

SQ Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other;

Query Match 100.0%; Score 1670; DB 19; Length 1670;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    301 tgctgagccggcgggacagccctgagcagcaccgacaccttcctgctccacctagctgtag 360

Qy    361 CAGACACGCTGCTGGTGTGACTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG 420
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Db    361 cagacacgctgctggtgctgacactgccgctctgggcagtggacgctgccgtccagtggg 420

Qy    421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480
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Db    421 tctttggctctggcctctgcaaagtggcaggtgccctcttcaacatcaacttctacgcag 480

Qy    481 GAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCACCC 540
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Db    481 gagccctcctgctggcctgcatacagctttgaccgctacctgaacatagttcatgccaccc 540

Qy    541 AGCTCTACCGCCGGGGGCCCCCGGCCCGCTGACCCCTACCTGCCTGGCTGTCTGGGGGC 600
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Db    541 agctctaccgcccgggggccccggcccgctgacctcacctgctggctgtctgggggc 600

Qy    601 TCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCTGTCGGCCCCACACGACGAGCGCC 660
          |||
Db    601 tctgctgcttttcgccctcccagacttcattctctgtcgccccaccacgacgagcgcc 660

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Db    661 tcaacgccaccactgccaatacaacttcccacaggtgggccgcacggctctgcggtgctgc 720

Qy    721 TGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCACACA 780
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Qy    781 TCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGCGCCTGCGGGCCATGCGGCTGGTGG 840
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Qy    841 TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGTGGTGG 900
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RN      [2]
RP      SEQUENCE OF 5-368 FROM N.A.
RX      MEDLINE; 96115583.
RA      Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
RA      Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA      O'Dowd B.F., Docherty J.M.;
RT      "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT      and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT      Y, and somatostatin receptors.";
RL      Genomics 29:335-344(1995).

```

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RN      [3]
RP      LIGAND BINDING.
RC      TISSUE=FETAL ASTROCYTES;
RX      MEDLINE; 98290735.
RA      Cole K.E., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
RA      Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
RA      Neote K.;
RT      "Interferon-inducible T cell alpha chemoattractant (I-TAC): A novel
RT      non-ELR CXC chemokine with potent activity on activated T cells
RT      through selective high affinity binding to CXCR3.";
RL      J. Exp. Med. 187:2009-2021(1998).
CC      !- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC.
CC      !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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DR EMBL; X95876; CAA65126.1; -.
DR EMBL; U32674; AAC50505.1; -.
DR GCRDB; GCR_1341; -.
DR GCRDB; GCR_1972; -.
DR MIM; 600894; -.
DR INTERPRO; IPR000276; -.
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 54 80 1 (POTENTIAL).
FT DOMAIN 81 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 90 110 2 (POTENTIAL).
FT DOMAIN 111 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 147 3 (POTENTIAL).
FT DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 170 189 4 (POTENTIAL).
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FT TRANSMEM 213 233 5 (POTENTIAL).
FT DOMAIN 234 255 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 256 277 6 (POTENTIAL).
FT DOMAIN 278 298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 321 7 (POTENTIAL).
FT DOMAIN 322 368 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 203 BY SIMILARITY.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POT
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POT
SQ SEQUENCE 368 AA; 40659 MW; F08A3B44B2BBAD04 CRC64;

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5/16/2022 COMMISSION

Query Match 100.0%; Score 1907; DB 1; Length 368;  
Best Local Similarity 100.0%; Pred. No. 1e-130;  
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPDFSLNFDRFLPALY 60  
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Db 1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPDFSLNFDRFLPALY 60

Sequenced comparison B

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Qy     121 SGLCKVAGALFNINFYAGALLLACISFDRLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180
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Db     121 SGLCKVAGALFNINFYAGALLLACISFDRLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180

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Db     181 LFLALPDFIFLSAHHDERLNATHCQYNFPQVGR TALRVLQLVAGFLLPLLVMAYCYAHILA 240

Qy     241 VLLVSRGQRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300
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Db     241 VLLVSRGQRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300

Qy     301 SVTSGLYGMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSET 360
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Db     301 SVTSGLYGMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSET 360

Qy     361 SEASYSGL 368
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Db     361 SEASYSGL 368

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# RESULT 4

CCR5\_HUMAN

ID CCR5\_HUMAN STANDARD; PRT; 372 AA.

AC P32302; Q14811;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXC-R5) (CXCR-5) (BURKITT'S LYMPHOMA

DE RECEPTOR 1) (MONOCYTE-DERIVED RECEPTOR 15) (MDR15).

GN BLR1 OR CXCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A. (LONG FORM).

RC TISSUE=LYMPHOCYTES;

RX MEDLINE; 93049615.

RA Dobner T., Wolf I., Emrich T., Lipp M.;

RT "Differentiation-specific expression of a novel G protein-coupled

RT receptor from Burkitt's lymphoma.";

RL Eur. J. Immunol. 22:2795-2799(1992).

RN [2]

RP SEQUENCE FROM N.A. (SHORT FORM).

RC TISSUE=BLOOD;

RX MEDLINE; 95366951.

RA Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;

RT "Sequence variation of a novel heptahelical leucocyte receptor

RT through alternative transcript formation.";

RL Biochem. J. 309:773-779(1995).

RN [3]

RP LIGAND BINDING.

RX MEDLINE; 98130629.

RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,

RA Baggiolini M., Moser B.;

RT "B cell-attracting chemokine 1, a human CXC chemokine expressed in

RT lymphoid tissues, selectively attracts B lymphocytes via

RT BLR1/CXCR5.";

RL J. Exp. Med. 187:655-660(1998).

CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BLR1 EXERTS

CC POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOMA (BL)

CC LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL

CC CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-

CC LYMPHOCYTES IN LYMPHATIC TISSUES.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.



Qy	245	SRGQRRRLRAMRLVVVVVAFALCWTPTYHLVLVDILMDLGALARNCGRESRVDVAKSVTS	304
		:   :   :   :           :   :     :   :   :	
Db	249	QRRPQKQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE	308
Qy	305	GLGYMHCCNLPLLYAFVGVKFRERMMWMLLLRLGCPNQRLQRPSSSRDSSWSSETSEAS	364
		:   :   :   :   :	
Db	309	FLGLAHCCNLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSWRR-SSLSESENAI	367



Qy	901	ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG	960
Db	901	acatcctcatggacctgggcgctttggcccgcaactgtggccgagaaagcagggtagacg	960
Qy	961	TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT	1020
Db	961	tggccaagtcggtcacctcaggcctgggctacatgcactgctgcctcaaccgctgctct	1020
Qy	1021	ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGC GCCTGGGCT	1080
Db	1021	atgcctttgtaggggtcaagttccgggagcggatgtggatgctgctcttgccgctgggct	1080
Qy	1081	GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGT	1140
Db	1081	gcccccaaccagagaggggtccagaggcagccatcgctctcccgccgggattcatcctggt	1140
Qy	1141	CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCTTTTCG	1200
Db	1141	ctgagacctcagaggcctcctactcgggcttgtgaggccggaatccgggctcccccttcg	1200
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Db	1201	cccacagtctgacttccccgcattccaggctcctccctccctctgccggtctggctctc	1260
Qy	1261	CCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAA	1320
Db	1261	cccaatatcctcgctcccggaactcactggcagccccagcaccaccagggtctcccgga	1320
Qy	1321	GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC	1380
Db	1321	gccaccctcccagctctgaggactgcaccattgctgctccttagctgccaaagccccatcc	1380
Qy	1381	TGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAACTTC	1440
Db	1381	tgccgcccgaggtggctgcctggagccccactgcccttctcatttggaaactaaacttc	1440
Qy	1441	ATCTTCCCCAAGTGC GGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCA	1500
Db	1441	atcttccccaaagtgcggggagtacaaggcatggcgtagaggtgctgccccatgaagcca	1500
Qy	1501	CAGCCCAGGCCTCCAGCTCAGCAGTGA CTGTGGCCATGGTCCCCAAGACCTCTATATTG	1560
Db	1501	cagcccaggcctccagctcagcagtgactgtggccatgggtccccaagacctctatattg	1560
Qy	1561	CTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAACAAGATCGTCAGG	1620
Db	1561	ctcttttattttatgtctaaatcctgcttaaaacttttcaataacaagatcgtcagg	1620
Qy	1621	ACCTTT	1670
Db	1621	accttt	1670

RESULT 2

T72800

ID T72800 standard; cDNA; 1876 BP.

XX

AC T72800;

XX

DT 28-SEP-1997 (first entry)

XX

DE Human G-protein chemokine receptor HSATU68 cDNA.

XX

KW HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;

KW signal transduction; gene therapy; diagnosis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 173..1420

FT /\*tag= a  
 FT primer\_bind complement (173..190)  
 FT /\*tag= b  
 FT primer\_bind 1402..1420  
 FT /\*tag= c  
 XX  
 PN WO9725340-A1.  
 XX  
 PD 17-JUL-1997.  
 XX  
 PF 11-JAN-1996; 96WO-US00499.  
 XX  
 PR 11-JAN-1996; 96WO-US00499.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Li Y;  
 XX  
 DR WPI: 1997-372810/34.  
 DR P-PSDB; W19780.  
 XX  
 PT DNA encoding new isolated human G-protein chemokine receptor - used  
 PT to develop products for treating, e.g. autoimmune diseases, chronic  
 PT infections, allergy, malignancy, inflammation or shock  
 XX  
 PS Claim 1; Fig 1a-d; 54pp; English.  
 XX  
 CC A cDNA clone (T72800) codes for a newly identified human G-protein  
 CC chemokine receptor (W19780) designated HSATU68. It was identified  
 CC in a human genomic library derived from activated T cells. HSATU68  
 CC nucleic acids be used to produce HSATU68 in prokaryotic or  
 CC eukaryotic host cells, as probes for the detection, screening and  
 CC diagnosis of diseases caused by mutations in the HSATU68 gene, and  
 CC in the gene therapy of conditions related to underexpression of the  
 CC receptor its ligand.  
 XX  
 SQ Sequence 1876 BP; 343 A; 625 C; 520 G; 388 T; 0 other;

Query Match 92.2%; Score 1540; DB 18; Length 1876;  
 Best Local Similarity 99.0%; Pred. No. 6.2e-287;  
 Matches 1549; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	58	CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG	117
Db	303	cctccccgttcccgccctcacaggtgagtgaccaccaagtgctaaatgacgccgaggttg	362
Qy	118	CCGCCCTCCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGA	177
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Qy	178	GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC	237
Db	423	gctgtacctccccgccctgcccacaggacttcagcctgaacttcgaccgggccttcctgc	482
Qy	238	CAGCCCTCTACAGCCTCCTCTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG	297
Db	483	cagccctcaacagcctcctcttctgctggggctgctgggcaacggcgcggtggcagccg	542
Qy	298	TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG	357
Db	543	tgctgctgagccggcgagacgccctgagcagcaccgacaccttctgctccacctagctg	602
Qy	358	TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT	417
Db	603	tagcagacacgctgctggtgctgacactgccgctctgggcagtggacgctgccgtccagt	662
Qy	418	GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG	477
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Qy	478	CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA	537
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Qy	538	CCCAGCTCTACCGCCGGGGCCCCCGGCCCGCTGACCTCACCTGCCTGGCTGTCTGGG	597
Db	783	cccagctctaccgcccggggccccggccgctgaccctcacctgcctggctgtctggg	842
Qy	598	GGCTCTGCCTGCTTTTCGCCCTCCAGACTTCATCTTCCTGTGCGCCACCACGACGAGC	657
Db	843	ggctctgctgcttttcgccctcccagacttcattctcctgtcggccaccacgacgagc	902
Qy	658	GCCTCAACGCCACCCACTGCCAATAACAATTCCACAGGTGGGCCGACGGCTCTGCGGG	717
Db	903	gcctcaacgcccaccactgccaataacaattccacaggtgggcccacggctctgcggg	962
Qy	718	TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCTACTGCTATGCCC	777
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Qy	1198	TCGCCCCACAGTCTGACTTCCCCGATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT	1257
Db	1443	tcgccccacagtctgacttccccgattccaggctcctccctccctctgccggctctggct	1502
Qy	1258	CTCCCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCACAGGTCTCCCGG	1317
Db	1503	ctccccaatatcctcgctcccgaggactcactggcagccccagcaccacaggtctcccg	1562
Qy	1318	GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA	1377
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Qy	1378	TCCTGCGCCCGGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAAC	1437
Db	1623	tcctgcgcccgagggtggctgcctggagccccactgcccttctcatttggaaactaaac	1682
Qy	1438	TTCATCTTCCCCAAGTGCGGGAGTACAAGGCATGGCGTAGAGGGTCTGCCCATGAAG	1497
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Qy	1498	CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT	1557
Db	1743	ccacagcccaggcctccagctcagcagtgactgtggccatggtccccaaagacctctatat	1802

Qy 1558 TTGCTCTTTTATTTTATGTCTAAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTC 1617  
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Qy 1618 AGGA 1621  
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Db 1863 agga 1866

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RESULT 1
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LOCUS HSGPCRIN8 1670 bp mRNA PRI 16-MAY-1997
DEFINITION H.sapiens mRNA for G-protein coupled receptor.
ACCESSION X95876
VERSION X95876.1 GI:1552845
KEYWORDS G protein-coupled receptor; interleukin-8 receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1670)
AUTHORS Loetscher,M., Gerber,B., Loetscher,P., Jones,S.A., Piali,L.,
Clark-Lewis,I., Baggiolini,M. and Moser,B.
TITLE Chemokine receptor specific for IP10 and mig: structure, function,
and expression in activated T-lymphocytes
JOURNAL J. Exp. Med. 184 (3), 963-969 (1996)
MEDLINE 97188912
REFERENCE 2 (bases 1 to 1670)
AUTHORS Loetscher,M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1996) M. Loetscher, Theodor-Kocher Institute,
University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
FEATURES
source Location/Qualifiers
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/db_xref="SWISS-PROT:P49682"
/translation="MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCP
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RRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVL
QLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVL
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polyA_signal 1602. .1607
polyA_site 1623
BASE COUNT 319 a 574 c 436 g 341 t
ORIGIN

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Query Match 97.2%; Score 1623; DB 66; Length 1670;  
Best Local Similarity 100.0%; Pred. No. 1.le-255;  
Matches 1623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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Qy 241 CCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGC 300  
|||||

Db 241 CCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGC 300

Qy 301 TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACACCTTCCTGCTCCACCTAGCTGTAG 360  
|||||

Db 301 TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCAGACACCTTCCTGCTCCACCTAGCTGTAG 360

Qy 361 CAGACACGCTGCTGGTGTGACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG 420  
|||||

Db 361 CAGACACGCTGCTGGTGTGACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG 420

Qy 421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480  
|||||

Db 421 TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG 480

Qy 481 GAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCACCC 540  
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Db 481 GAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGCCACCC 540

Qy 541 AGCTCTACCGCCGGGGGCCCCGGCCCCGCGTGACCCCTACCTGCCTGGCTGTCTGGGGGC 600  
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Db 541 AGCTCTACCGCCGGGGGCCCCGGCCCCGCGTGACCCCTACCTGCCTGGCTGTCTGGGGGC 600

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Db 601 TCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTGCGCCACACGACGAGCGCC 660

Qy 661 TCAACGCCACCCACTGCCAATACAACCTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGC 720  
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Db 661 TCAACGCCACCCACTGCCAATACAACCTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGC 720

Qy 721 TGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCCTACTGCTATGCCACACA 780  
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Db 721 TGCAGCTGGTGGCTGGCTTTCTGCTGCCCTGCTGGTCATGGCCTACTGCTATGCCACACA 780

Qy 781 TCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCCCTGCGGGCCATGCGGCTGGTGG 840  
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Db 781 TCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCCCTGCGGGCCATGCGGCTGGTGG 840

Qy 841 TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGTGG 900  
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Db 841 TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGTGG 900

Qy 901 ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG 960  
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Db 901 ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG 960

Qy 961 TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT 1020  
|||||

Db 961 TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT 1020

Qy 1021 ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCT 1080  
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Db 1021 ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCT 1080

Qy 1081 GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGT 1140  
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Db 1081 GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGT 1140

Qy 1141 CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCG 1200  
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Db 1141 CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCG 1200

Qy 1201 CCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC 1260  
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Db 1201 CCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC 1260

Qy 1261 CCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAA 1320

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Db 1261 CCCAATATCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACACCAGGTCTCCCGGGAA 1320
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Db 1321 GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC 1380
Qy 1381 TGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTGGAAACTAAACTTC 1440
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Qy 1441 ATCTTCCCCAAGTGCAGGGAGTACAAGGCATGGCGTAGAGGGTGTGCCCCATGAAGCCA 1500
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Qy 1501 CAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTG 1560
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Qy 1621 ACC 1623
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Db 1621 ACC 1623

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RESULT 2

HSXDP\_4/c

WPCOMMENT

Sequence split into 6 fragments LOCUS HSXDP Accession AJ239319

Fragment Name	Begin	End
HSXDP_0	1	110000
HSXDP_1	100001	210000
HSXDP_2	200001	310000
HSXDP_3	300001	410000
HSXDP_4	400001	510000
HSXDP_5	500001	547722

Continuation (5 of 6) of HSXDP from base 400001 (AJ239319 Homo sapiens chromosome X clone cosmid cosE3 map Xq13.1, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 ordered pieces. 5/2000)

Query Match 92.5%; Score 1545.2; DB 90; Length 110000;  
 Best Local Similarity 99.2%; Pred. No. 3e-243;  
 Matches 1553; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177
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Db 38001 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 37942
Qy 178 GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACCTCGACCGGGCCTTCCTGC 237
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Db 37941 GCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACCTCGACCGGGCCTTCCTGC 37882
Qy 238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297
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Db 37881 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 37822
Qy 298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357
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Db 37821 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 37762
Qy 358 TAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417
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Db 37761 TAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 37702

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Qy 478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537  
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 Db 37641 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 37582

Qy 538 CCCAGCTCTACCGCCGGGGGCCCCGGCCCGCTGACCCCTACCTGCCTGGCTGTCTGGG 597  
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07607186

SLQ ID no: 2

RESULT 1  
W54371  
ID W54371 standard; Protein; 368 AA.  
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AC W54371;  
XX  
DT 14-AUG-1998 (first entry)  
XX  
DE Human IP-10/Mig receptor CXCR3 protein.  
XX  
KW chemokine receptor; cellular signal; treatment; T cell; antitumour;  
KW antiviral; inflammatory disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT Modified-site 32  
FT /note= "N-linked glycosylation site"  
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FT Domain 127..147  
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FT Domain 302..322  
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PN WO9811218-A1.  
XX  
PD 19-MAR-1998.  
XX  
PF 10-SEP-1997; 97WO-US15915.  
XX  
PR 31-MAR-1997; 97US-0829839.  
PR 10-SEP-1996; 96US-0709838.  
XX  
PA (KOCH-) KOCHER INST THEODOR.  
PA (LEUK-) LEUKOSITE INC.  
XX  
PI Loetscher M, Mackay CR, Moser B, Qin S;  
XX  
DR WPI; 1998-207381/18.  
DR N-PSDB; V26557.  
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PT DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of  
PT which, are useful for treatment of inflammation or in anti-tumour or  
PT anti-viral therapy  
XX  
PS Claim 7; Fig 2; 137pp; English.  
XX  
CC The mammalian CXC chemokine receptor 3 (CXCR3) protein can selectively  
CC bind one or more chemokines and can mediate cellular signalling and/or a  
CC cellular response in response. Inhibitors and promoters of mammalian  
CC CXCR3 can be detected and identified using host cells expressing CXCR3.  
CC CXCR3 inhibitors can be used for treatment of inflammatory diseases which  
CC are T cell mediated. CXCR3 promoters are useful for antitumour or  
CC antiviral therapy.  
XX  
SQ Sequence 368 AA;

Query Match 100.0%; Score 1907; DB 19; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-217;  
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 SLLFLLGLLNGGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTPLPLWAVDAAVQWVFG 120
      |||
Db     61 slflglgllnggavaavllsrrtalsstdtflhlavadtllvltplplwavdaavqwvfg 120

Qy    121 SGLCKVAGALFNINFYAGALLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180
      |||
Db    121 sgckvagalfninfyagalllacisfdrylnivhatqlyrrgpparvlttclavwglcl 180

Qy    181 LFALPDFIFLSAHHDERLNATHCQYNFPQVGRTRALRVLQLVAGFLLPLLVMAYCYAHILA 240
      |||
Db    181 lfalpdfiflsahhderlnathcqynfpqvgtralrvlqlvagfllpllvmaycyahila 240

Qy    241 VLLVSRGQRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300
      |||
Db    241 vllvsrgqrllramrlvvvvvafalcwtpyhlvvlvdilmdlgalarncgresrvdvak 300

Qy    301 SVTSGLYGMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRPSSSRDSSWSET 360
      |||
Db    301 svtsglygmhcclnpllyafvgvkfrermwmlllrlgcpnqrqlrqpsssrrdsswset 360

Qy    361 SEASYSGL 368
      |||
Db    361 seasysgl 368
  
```

RESULT 6

R27793

ID R27793 standard; Protein; 372 AA.

XX

AC R27793;

XX

DT 12-MAR-1993 (first entry)

XX

DE New platelet factor 4 receptor superfamily member PF4ARii.

XX

KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;

KW pro-inflammatory cytokine; 8rr.9.

XX

OS Homo sapiens.

XX

PN WO9217497-A.

XX

PD 15-OCT-1992.

XX

PF 23-MAR-1992; 92WO-US02317.

XX

PR 29-MAR-1991; 91US-0677211.

PR 19-DEC-1991; 91US-0810782.

XX

PA (GETH ) GENENTECH INC.

XX

PI Holmes WE, Lee J, Wood WI;

XX

DR WPI; 1992-366191/44.

DR N-PSDB; Q37107.

XX

PT Isolated human platelet factor 4 super-family receptor

PT polypeptide and corresp. antibodies and DNA - useful as

PT diagnostic and screening agents, and for treating inflammation or

PT PF4AR-mediated disorders

XX



A;Molecule type: mRNA  
A;Residues: 151-269 <WIL>  
A;Cross-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.6%; Score 640; DB 2; Length 374;  
Best Local Similarity 40.9%; Pred. No. 3.5e-50;  
Matches 143; Conservative 54; Mismatches 139; Indels 14; Gaps 6;

Qy 23 FSSSYDYGENESDSCCTSPPCQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 82  
:|:| : :|:| :| :| :|:|:|:|:| :| :| :|  
Db 26 YNSTEIPQLQDSNFCST---VEGPLLTSEKAVFMPVAYSILFLLGMMGNILVLVILERHR 82

Qy 83 TALSSDTDFLLHLAVADTLLVLTPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 142  
|:|:|:| :|:|:| :| :| :| :|:| :| :| :|:| :|:| :|:|  
Db 83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGVWLTGFLCKTVIALHKINIFYCSSLLV 142

Qy 143 ACISFDRLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFAIPDFIFLSA---HHDERLN 199  
|:|:| :|:| :|:| :| :| :| :|:| :| :| :|:| :| :|:| :|  
Db 143 ACIAVDRLAIVHAVHAYRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDL- 201

Qy 200 ATHCQYNFPQVGR-----ALRVLQVLVAGFLPLLVLMAYCYAHILAVLL-VSRGQRRRLRAM 254  
| : : | : | : |:|:|:| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 202 -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLQAQRRPQRQKAV 260

Qy 255 RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGVMHCCLN 314  
| : :| :|:|:|:|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 261 RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy 315 PLYAFYGVGKFRERMWMLLLRLGCPNQRGLQRQPSSRRDSSWSETSEAS 364  
|:|:| :|:|:| :| :|:| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 321 PMLYTFAGVKFRSDLSRLLTCLGCAGPASL-CQLFPNWRKSSLSSEENAT 369

RESULT 5  
A53611  
interleukin-8 receptor type B - human  
C;Species: Homo sapiens (man)  
C;Date: 07-Oct-1994 #sequence\_revision 12-Apr-1996 #text\_change 05-Nov-1999  
C;Accession: I37898; I38712; A53611; A39446  
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.  
J. Biol. Chem. 269, 26381-26389, 1994  
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.  
A;Reference number: I37898; MUID:95014476  
A;Accession: I37898  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-360 <RES>  
A;Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803  
A;Accession: I38712  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15 <RE2>  
A;Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873;  
NID:g511810; PID:g511811; EMBL:U11874; NID:g511812; PID:g511813; EMBL:U11875;  
NID:g511814; PID:g511815; EMBL:U11876; NID:g511816; PID:g511817; EMBL:U11877;  
NID:g511818; PID:g511819; EMBL:U11878; NID:g511820; PID:g511821  
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.  
J. Biol. Chem. 269, 11065-11072, 1994  
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.  
A;Reference number: A53611; MUID:94209273  
A;Accession: A53611  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 6-360 <SPR>

A;Cross-references: GB:M99412; GB:L19593  
R;Murphy, P.M.; Tiffany, H.L.  
Science 253, 1280-1283, 1991  
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.  
A;Reference number: A39446; MUID:91368200  
A;Accession: A39446  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 6-360 <MUR>  
A;Cross-references: GB:M73969  
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including GRO, NAP-2, and ENA-78.  
C;Genetics:  
A;Gene: GDB:IL8RB; IL8RA  
A;Cross-references: GDB:127868; OMIM:146928  
A;Map position: 2q35-2q35  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 633; DB 2; Length 360;  
Best Local Similarity 40.1%; Pred. No. 1.4e-49;  
Matches 141; Conservative 51; Mismatches 130; Indels 30; Gaps 6;

Qy	25	SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA	84
		:    :     :     :     :	
Db	21	SNYSYSTLPPFLDAAPEPE-SLEINKYFVVIYALVFLSLLGNSLVMVLVILYSRVG	79
Qy	85	LSSTDTFLHLAVADTLLVLTPLWAVDAVQWVFGSGLCKVAGALFNINFYAGALLLAC	144
		:     :	
Db	80	RSVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVVSLLEKVNIFYSGILLAC	139
Qy	145	ISFDRLNIVHATQLYRRGPPARVTLT-----CLAVWGLCLLFALPDFIFLSAHHD	195
		:	
Db	140	ISVDRYLAIVHATR-----TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS	189
Qy	196	ERLNATHCQYNFPQVG-----RTALRVLQVLVAGFLLPLLVMAYCYAHILAVLLVSRGQR	249
		: :   : :	
Db	190	SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLCYGFTRLTLFKAHMGQ	245
Qy	250	RLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGVM	309
		:         :     :	
Db	246	KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVQETCERRNHIDRALDATEILGIL	305
Qy	310	HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSETS	361
		:         :       :	
Db	306	HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPRKDSRPSFVGSSSGHTS	357

RESULT 1  
CCR3\_HUMAN  
ID CCR3\_HUMAN STANDARD; PRT; 368 AA.  
AC P49682;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE C-X-C CHEMOKINE RECEPTOR TYPE 3 (CXC-R3) (CXCR-3).  
GN CXCR3 OR GPR9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BLOOD;  
RX MEDLINE; 97188912.  
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,  
RA Clark-Lewis I., Baggiolini M., Moser B.;  
RT "Chemokine receptor specific for IP10 and mig: structure, function,  
RT and expression in activated T-lymphocytes."  
RL J. Exp. Med. 184:963-969(1996).